Amendments to the Specification:

Please replace the paragraph beginning at page 4, line 29, with the following:

--Figure 5 shows the nucleotide (SEQ ID NO:8) and deduced amino acid sequence ~~(SEQ ID NO:9)~~ (SEQ ID NOS:9-11) of the *AGL9* cDNA.--

Please replace the paragraph beginning at page 4, line 31, with the following:

--Figure 6a through 6f shows the *Arabidopsis AP1* promoter ~~SEQ ID NO: 10~~ SEQ ID NO:12.--

Please replace the paragraph beginning at page 4, line 32, with the following:

--Figure 7 shows a diagram of reporter construct POP10. The construct has 1.7 kb *AP1* promoter plus the entire coding region of *AP1* in front of promoterless GUS gene in pBI101.2 plasmid. The construct has 1.7 kb *AP1* promoter plus the entire coding region of *AP1* in front of promoterless GUS gene in pBI101.2 plasmid. The construct was first made by PCR amplification from intron 3 to the end of *AP1* gene in exon 8 (right before stop codon) using KY65 plasmid containing *AP1* genomic region as template. The HindIII site was added to the forward primer AP1HIN [5'-CAAGCTTGTACACATTTACACTCATCACAT-3' (SEQ ID NO:17)] and BamHI site was added to reverse primer AP1BAM, [5'-CGGATCCTGCGCGAAGCAGCCAAGGTTG-3' (SEQ ID NO:18)] to aid cloning (sequence in italic are restriction sites of HindIII and BamHI). The 1.7 kb amplified fragment was cloned into plasmid pBI101.2 using HindIII and BamHI sites giving construct POP9. The 3.6 kb HindIII

/ XbaI fragment was isolated from KY65 plasmid and cloned into POP9 construct giving POP10 construct.--

Please replace the paragraph beginning at page 5, line 12, with the following:

--Figure 8a through 8b shows the nucleotide ~~(SEQ ID NO:11)~~ (SEQ ID NO:13) and deduced amino acid sequence ~~(SEQ ID NO:12)~~ (SEQ ID NO:14) of the *AP1* cDNA.--

Please replace the paragraph beginning at page 5, line 17, with the following:

--Figure 10a through 10b shows the nucleotide ~~(SEQ ID NO:6)~~ (SEQ ID NO:15) and amino acid sequence (SEQ ID NO:7) of the *AGL4* cDNA.--

Please replace the paragraph beginning at page 5, line 19, with the following:

--Figure 11a through 11b shows the nucleotide ~~(SEQ ID NO:4)~~ (SEQ ID NO:16) and amino acid sequence (SEQ ID NO:5) of the *AGL2* cDNA.--

Please replace the paragraph beginning at page 15, line 3, with the following:

--As used herein the term "*AP1* regulatory element" refers to a regulatory element derived from ~~Arabidopsis~~ *Arabidopsis AP1* ~~(SEQ ID NO:10)~~ (SEQ ID NO:12) or an ortholog of *Arabidopsis AP1*. An *AP1* ortholog is a MADS box gene product expressed, at least in part, in one or more floral organs of a plant and having homology to the amino acid sequence of *Arabidopsis AP1* ~~(SEQ ID NO:10)~~ (SEQ ID NO:12). An *AP1* ortholog can be, for example, a snapdragon ortholog, such as SQUAMOSA. Also, an *AP1* ortholog could be, for example, a

Eucalyptus, pine or spruce ortholog. An *AP1* ortholog generally has at least about 75% amino acid identity with amino acids 1 to 160 of *Arabidopsis AP1* ~~(SEQ ID NO:10)~~ (SEQ ID NO:12) and can have, for example, at least about 85%, 90%, or 95% amino acid identity with amino acids 1 to 160 of *Arabidopsis AP1* ~~(SEQ ID NO:10)~~ (SEQ ID NO:12).--

Please replace the paragraph beginning at page 15, line 20, with the following:

--An *AGL2*, *AGL4* or *AGL9* or *AP1* floral organ selective regulatory element also can be introduced into a heterologous plant to produce a transgenic plant of the invention characterized by suppressed flowering. AGAMOUS-like gene products have been widely conserved throughout the plant kingdom; for example, AGAMOUS has been conserved in tomato (TAG1) and maize (ZAG1), indicating that orthologs of AGAMOUS-like genes are present in most, if not all, angiosperms (Pnueli et al., The Plant Cell 6:163-173 (1994); Schmidt et al., The Plant Cell 5:729-737 (1993)). Furthermore, it has been shown that MADS-box genes exist in gymnosperms and angiosperms as well as in ferns, the common ancestors of contemporary seed plants (Tandre et al., Plant Mol. Biol. 27:69-78 (1995); Liu and Podila, Plant Phys. 113:665 (1997); Münster et al., Proc. Natl. Acad. Sci., IJSA 94:2145-2420 (1997); and Mouradov et al., Plant Physiol. 117:55-62 (1998)). *AGL2*, *AGL4* and *AGL9* floral organ selective regulatory elements also can be conserved and can function across species boundaries to confer floral organ selective expression in heterologous plant species. Thus, an *Arabidopsis AGL2*, *AGL4* or *AGL9* or *AP1* floral organ selective regulatory element, such as the *Arabidopsis AGL2*, *AGL4* or *AGL9* or *AP1* promoter SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:3 or ~~(SEQ ID NO: 10)~~ (SEQ ID NO:12), or an active fragment thereof, can confer floral organ selective expression upon an operatively linked nucleotide sequence encoding a cytotoxic gene product in a heterologous plant such as *Eucalyptus*, whereby the cytotoxic gene product is selectively expressed in floral tissue and flowering is suppressed.--

Please replace the paragraph beginning at page 18, line 7, with the following:

--The *Arabidopsis AP1* promoter ~~(SEQ ID NO:10)~~ (SEQ ID NO:12) is shown in Figure 6. An *AP1* regulatory element, such as a 5' regulatory element or intronic regulatory element, can confer selective expression in one or more floral organs, specifically in petals, stamens and carpels, and, thus, is a floral organ selective regulatory element as defined herein. An isolated *AP1* floral organ selective regulatory element can have, for example, at least fifteen contiguous nucleotides of the *Arabidopsis AP1* sequence ~~(SEQ ID NO:10)~~ (SEQ ID NO:12). Such an isolated *AP1* floral organ selective regulatory element can have, for example, at least 16, 18, 20, 25, 30, 40, 50, 100 or 500 contiguous nucleotides of ~~(SEQ ID NO:10)~~ (SEQ ID NO:12) and is characterized, in part, by the ability to confer floral organ selective expression upon an operatively linked nucleotide sequence (see Example IV).--

Please replace the paragraph beginning at page 27, line 14, with the following:

--The entire 1.7 kb *AP1* promoter shown in Figure 6 ~~(SEQ ID NO: 10)~~ (SEQ ID NO:12) plus the entire coding region of *AP1* including introns was cloned into the GUS expression vector pBI101.2 to produce the POP10 construct (Figure 7). The construct was first made by PCR amplification from intron 3 to the end of *AP1* gene in exon 8 (right before stop codon) using KY65 plasmid containing *AP1* genomic region as template. The HindIII site was ~~addded~~ added to the forward primer AP1HIN and BamHI site was added to reverse primer AP1BAM to aid cloning. The 1.7 kb amplified fragment was cloned into plasmid pBI101.2 using HindIII and BamHI sites giving construct POP9. The 3.6 kb HindIII / XbaI fragment was isolated from KY65 plasmid and cloned into POP9 contruct giving POP10 contruct.--

Please cancel the present "SEQUENCE LISTING", pages 1-21, submitted for parent application PCT/US99/24407 on February 22, 2000, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to 21, at the end of the application.